Amendments to the Claims:

The following listing of claims will replace all prior versions, and listings, of claims in the application.

1. (*Currently amended*) A method for managing a plurality of databases containing gene expression data and related data corresponding to a plurality of gene fragments, the method comprising:

storing the gene expression data in a gene expression database, wherein the gene expression data is obtained from microarrays;

storing the related data in separate databases comprising a sample database and a gene ~~annotation~~ fragment index database;

grouping the plurality of gene fragments into at least two gene fragment classes according to at least one attribute of a plurality of attributes of the gene expression data and related data, the plurality of attributes selected from the group consisting of sample data, gene ~~annotation~~ fragment index data, experiment data, and expression results, wherein the sample data resides in the sample database and includes information corresponding to one or more of clinical data, donor, organ, tissue, disease, pathology, genomics, medications and preparation, wherein the gene ~~annotation~~ fragment index data resides in the gene ~~annotation~~ fragment index database and includes one or more of known versus unknown standardized identifier, gene fragment identity, gene sequence, gene pathway and chromosome location, and wherein expression results include information corresponding to one or more of call value, expression level, fold change, up-regulated versus down-regulated; and

using a relational format, generating a plurality of links between the gene expression database and the separate databases for linking the gene expression data for each gene fragment to the at least one attribute corresponding to the gene fragment class into which the gene fragment is grouped;

wherein a user query comprising a selection of one or a combination of attributes produces a result comprising a subset of the gene expression data and the related data corresponding to one or more gene fragment classes having the selected one or a combination of attributes.

Claims 2-15 (*Canceled*)

16. (*Currently amended*) The method of Claim 1, wherein the selection of one or more of a combination of attributes comprises:

selecting one or a combination of attributes of the gene ~~annotation~~ fragment index data to define a gene set; and

selecting one or a combination of attributes of the sample data to define one or more sample sets;

wherein the result comprises a ranking of the expression levels for each gene fragment within the gene set across the one or more sample sets.

17. (*Previously presented*) The method of Claim 1, wherein the selection of one or a combination of attributes comprises defining a sample set and specifying a call value threshold, wherein the result comprises a gene signature analysis to identify a pair of gene sets comprising present genes and absent genes within the sample set.

18. (*Previously presented*) The method of Claim 17, further comprising storing the result in a workspace manager, wherein the selection of one or more attributes further comprises:

defining a second sample set and the call value threshold to perform a second gene signature analysis; and

comparing the results for the first and second sample sets to produce a gene signature differential analysis.

19. (*Previously presented*) The method of Claim 1, wherein the selection of one or a combination of attributes comprises:

defining each of a control sample set and an experimental sample set; and

comparing expression levels for the control sample set and experimental sample set to produce a fold change analysis.

20. (*Previously presented*) The method of Claim 19, wherein the selection of one or a combination of attributes further comprises selecting an additional attribute corresponding to a fold change value threshold.

21. (*Currently amended*) A system for managing a plurality of databases containing gene expression data and related data corresponding to a plurality of gene fragments, the system comprising:

an analysis engine;

a gene expression database for storing the gene expression data, wherein the gene expression data is obtained from microarrays;

separate databases comprising a sample database and a gene ~~annotation~~ fragment index database for storing the related data;

a common interface for linking the gene expression data and the related data by:

grouping the plurality of gene fragments into at least two gene fragment classes according to at least one attribute of a plurality of attributes of the gene expression data and related data, the plurality of attributes selected from the group consisting of sample data, gene ~~annotation~~ fragment index data, experiment data, and expression results, wherein sample data resides in the sample database and includes information corresponding to one or more of clinical data, donor, organ, tissue, disease, pathology, genomics, medications and preparation, wherein gene ~~annotation~~ fragment index data resides in the gene ~~annotation~~ fragment index database and includes one or more of known versus unknown standardized identifier, gene fragment identity, gene sequence, gene pathway and chromosome location, and wherein expression results include information corresponding to one or more of call value, expression level, fold change, up-regulated versus down-regulated; and

using a relational format, generating a plurality of links between the gene expression database and the at least one separate database for associating the gene expression data for each gene fragment to the at least one attribute corresponding to the gene fragment class into which the gene fragment is grouped; and

a user interface for entry of a user query and reporting of a result, wherein the user query comprises a selection of one or a combination of attributes for directing the analysis engine to search the gene expression database and the at least one separate data database for a

subset of the gene expression data and the related data corresponding to one or more gene fragment classes having the selected one or a combination of attributes.

22-23. (*Canceled*)

24. (*Currently amended*) The system of Claim 22, wherein the user query comprises:

selecting one or a combination of attributes of the gene ~~annotation~~ fragment index data to define a gene set; and

selecting one or a combination of attributes of the sample data to define one or more sample sets;

wherein the result comprises a ranking of the expression levels for each gene fragment within the gene set across the one or more sample sets.

25. (*Previously presented*) The system of Claim 21, wherein the user query comprises selection of a combination of attributes to define a sample set and to specify a call value threshold, wherein the result comprises a gene signature analysis to identify a pair of gene sets comprising present genes and absent genes within the sample set.

26. (*Previously presented*) The system of Claim 25, further comprising a workspace manager for storing the result, wherein the user query further comprises:

defining a second sample set and the call value threshold to perform a second gene signature analysis; and

comparing the results for the first and second sample sets to produce a gene signature differential analysis.

27. (*Previously presented*) The system of Claim 21, wherein the user query comprises:

selecting one or a combination of attributes defining each of a control sample set and an experimental sample set; and

comparing expression levels for the control sample set and experimental sample set to produce a fold change analysis.

28. (*Previously presented*) The system of Claim 27, wherein user query further comprises selection of an additional attribute corresponding to a fold change value threshold.

Claims 29-34 (*Canceled*)

35. (*Currently amended*) A system for managing a plurality of databases containing data corresponding to a plurality of gene fragments, the plurality of databases comprising:

a gene expression database for storing the gene expression data corresponding to the plurality of gene fragments, wherein the gene expression data is obtained from microarrays;

a sample database for storing sample data corresponding to the gene expression data; and

a gene ~~annotation~~ fragment index database for storing gene ~~annotation~~ fragment index data corresponding to the gene expression data;

wherein the gene expression database, the sample database and the gene ~~annotation~~ fragment index database are linked by grouping the plurality of gene fragments into at least two gene fragment classes according to at least one attribute of a plurality of attributes of the gene expression data and related data, the plurality of attributes selected from the group consisting of sample data, gene ~~annotation~~ fragment index data, experiment data, and expression results, wherein sample data includes information corresponding to one or more of clinical data, donor, organ, tissue, disease, pathology, genomics, medications and preparation, wherein gene ~~annotation~~ fragment index data includes one or more of known versus unknown standardized identifier, gene fragment identity, gene sequence, gene pathway and chromosome location, and wherein expression results include information corresponding to one or more of call value, expression level, fold change, up-regulated versus down-regulated; and wherein a user query entered into the network system comprises a selection of one or a combination of attributes for searching the gene expression database, the sample database and the gene ~~annotation~~ fragment index database for a subset of the gene expression data and the sample data and the gene ~~annotation~~ fragment index data corresponding to one or more gene fragment classes having the selected one or a combination of attributes.

36. (*Canceled*)

37. (*Currently amended*) The system of Claim 35, wherein the user query comprises:

selecting one or a combination of attributes of the gene ~~annotation~~ <u>fragment index</u> data to define a gene set; and

selecting one or a combination of attributes of the sample data to define one or more sample sets;

wherein the result comprises a ranking of the expression levels for each gene fragment within the gene set across the one or more sample sets.

38. (*Previously presented*) The system of Claim 35, wherein the user query comprises selection of a combination of attributes to define a sample set and to specify a call value threshold, wherein the result comprises a gene signature analysis to identify a pair of gene sets comprising present genes and absent genes within the sample set.

39. (*Previously presented*) The system of Claim 38, further comprising a workspace manager for storing the result, wherein the user query further comprises:

defining a second sample set and the call value threshold to perform a second gene signature analysis; and

comparing the results for the first and second sample sets to produce a gene signature differential analysis.

40. (*Previously presented*) The system of Claim 35, wherein the user query comprises:

selecting one or a combination of attributes defining each of a control sample set and an experimental sample set; and

comparing expression levels for the control sample set and experimental sample set to produce a fold change analysis.

41. (*Previously presented*) The system of Claim 40, wherein user query further comprises selection of an additional attribute corresponding to a fold change value threshold.